

Amendments to the Claims:

The following listing of claims will replace all prior versions, and listings, of claims in the application:

1.-15. (Canceled)

16. (New) An isolated oligonucleotide consisting of a sequence selected from the group consisting of SEQ ID NO: 1 to SEQ ID NO: 4 and sequences complementary thereto, wherein "n" represents inosine.

17. (New) A mixture of 64 isolated oligonucleotides each consisting of a sequence selected from the group consisting of SEQ ID NO: 1 to SEQ ID NO: 4 and sequences complementary thereto, wherein "n" represents an equimolar mixture of the nucleotides a, t, c and g.

18. (New) A method to determine whether bacteria belonging to the order of Spirochaetales is present in a sample containing or likely to contain nucleic acid from said bacteria, comprising:

(a) contacting said sample with at least one probe comprising an oligonucleotide according to claim 16; and

(b) determining whether a hybridization complex forms between said at least one probe and said nucleic acid in said sample.

19. (New) A method according to claim 18, wherein said oligonucleotide is immobilised on a solid support.

20. (New) A method according to claim 18, wherein said oligonucleotide is marked with a tracing agent.

21. (New) A method to determine whether bacteria belonging to the order of Spirochaetales is present in a sample containing or likely to contain nucleic acid from said bacteria, comprising:

(a) contacting said sample with at least one probe comprising a mixture of oligonucleotides according to claim 17; and

(b) determining whether a hybridization complex forms between said at least one probe and said nucleic acid in said sample.

22. (New) A method according to claim 21, wherein said oligonucleotides are immobilised on a solid support.

23. (New) A method according to claim 21, wherein said oligonucleotides are marked with a tracing agent.

24. (New) A method to determine whether bacteria belonging to the order of Spirochaetales is present in a sample containing or likely to contain nucleic acid from said bacteria, comprising:

(a) contacting said sample with primers comprising oligonucleotides according to claim 16;

(b) carrying out an amplification; and

(c) determining the presence or absence of an amplification product.

25. (New) A method to determine whether bacteria belonging to the order of Spirochaetales is present in a sample containing or likely to contain nucleic acid from said bacteria, comprising:

(a) contacting said sample with primers comprising mixtures of oligonucleotides according to claim 17;

(b) carrying out an amplification; and

(c) determining the presence or absence of an amplification product.

26. (New) A method according to claim 24 or 25, further comprising:

(d) sequencing the amplified fragment when an amplification product is obtained; and

(e) comparing the sequence of the amplified fragment with the known sequence of gene *rpoB* of the bacteria, wherein the species of the bacteria is determined if the sequence of the amplified fragment is identical to that of the known sequence.